

EXHIBIT 3

1: Mol Microbiol. 1993 Feb;7(4):505-14.

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Class 1 outer membrane protein of *Neisseria meningitidis*: epitope analysis of the antigenic diversity between strains, implications for subtype definition and molecular epidemiology.

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The VR1 and VR2 regions of the class 1 protein have been sequenced from a number of meningococcal strains, including non-subtypable strains and strains of apparently identical subtype. The amino acid sequences have been used to construct synthetic peptides for mapping subtype-specific epitopes. The majority of epitopes was found to be located in VR2 at the apex of a predicted surface-exposed loop. A single amino acid change within an epitope, or an amino acid deletion outside an epitope, were both associated with loss of subtype specificity, resulting from a change in the predicted conformation at the apex of the loop structure. Analysis of the sequence information combined with knowledge of defined epitopes also revealed considerable additional information not demonstrated by current subtyping procedures.

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